

55. The polynucleotide of Claim 53, which is SEQ ID NO: 1.
56. A vector comprising the polynucleotide of Claim 53.
57. A microorganism transformed with the vector of Claim 56.
58. A method of producing a protein which has the activity of SEQ ID NO: 2, comprising culturing the transformed microorganism of Claim 57 under conditions suitable to produce the protein.
59. An isolated polynucleotide from *Corynebacterium glutamicum* which hybridizes under stringent conditions to SEQ ID NO: 1 or the full complement of SEQ ID NO: 1, wherein the stringent conditions comprise washing in 5X SSC at a temperature from 50 to 68°C, and wherein the polynucleotide encodes a protein having the activity of SEQ ID NO: 2.
60. A vector comprising the polynucleotide of Claim 53.
61. A microorganism transformed with the vector of Claim 60.
62. A method of producing a protein which has the activity of SEQ ID NO: 2, comprising culturing the transformed microorganism of Claim 61 under conditions suitable to produce the protein.
63. An isolated polynucleotide consisting of 30 to 383 consecutive nucleotides of SEQ ID NO: 1.
64. An isolated polynucleotide consisting of at least 30 consecutive nucleotides of SEQ ID NO: 1.
65. The polynucleotide of Claim 64, which is SEQ ID NO: 3.
66. A vector comprising the polynucleotide of Claim 64.
67. The vector of Claim 66, wherein the polynucleotide is SEQ ID NO: 3.

68. The vector of Claim 66, which is pCR2.1lysR1int shown in Figure 1 and deposited as DSM 13616 at the German Collection for Microorganisms and Cell Cultures (DSMZ, Brunswick, Germany).

69. *Escherichia coli* TOP10F/pCR2.1lysR1int deposited as DSM 13616 at the German Collection for Microorganisms and Cell Cultures (DSMZ, Brunswick, Germany).

70. A *coryneform* bacterium which comprises an attenuated lysR1 gene.

71. The *coryneform* bacterium of Claim 70, wherein the lysR1 gene comprises the polynucleotide sequence of SEQ ID NO:1.

72. *Escherichia coli* DSM 13616.

73. A process for producing L-amino acids, comprising culturing a bacterial cell in a medium suitable for producing L-amino acids, wherein the bacterial cell comprises an attenuated lysR1 gene.

74. The process of Claim 73, wherein the bacterial cell is a *coryneform* bacterium or *Brevibacterim*.

75. The process of Claim 74, wherein the bacterial cell is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, *Brevibacterium divaricatum*.

76. The process of Claim 75, wherein the lysR1 gene comprises the polynucleotide sequence of SEQ ID NO: 1.

77. The process of Claim 73, wherein said L-amino acid is L-lysine.

78. The process of Claim 73, wherein said L-amino acid is L-valine.

79. The process of Claim 73, wherein said bacteria further comprise at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of dapA, eno, zwf, pyc, and lysE.

80. The process of Claim 73, wherein said bacteria further comprise at least one gene whose expression is attenuated, wherein said gene is selected from the group consisting of pck, pgi, and poxB.

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81. An isolated polynucleotide which comprises the full complement of nucleotides 201-1109 of SEQ ID NO: 1,

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82. The polynucleotide of Claim 81, which is the full complement of SEQ ID NO: 1.

SUPPORT FOR THE AMENDMENTS

Newly-added Claims 53-82 are supported by the specification at pages 2-27 and by original Claims 1-39. No new matter is believed to have been added to this application by these amendments.

REMARKS

Claims 53-82 are pending. Favorable reconsideration is respectfully requested.

The rejection under 35 U.S.C. § 112, first paragraph, is believed to be obviated by the amendment submitted above in part and is, in part, respectfully traversed.

Claim 53 is directed to an isolated polynucleotide from *Corynebacterium* which encodes a protein comprising the amino acid sequence of SEQ ID NO: 2, where the protein has the activity of SEQ ID NO: 2.